

9904247_1.Dna /rev

Emfun:Scl9354

ID SCL9354 standard; DNA; FUN; 15693 BP.
AC U53878; Y13138;
SV U53878.1
DT 10-APR-1996 (Rel. 47, Created)
DT 23-AUG-1997 (Rel. 52, Last updated, Version 3)

DE Saccharomyces cerevisiae chromosome XII cosmid 9354.
KW .
OS Saccharomyces cerevisiae (baker's yeast)
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP 1-15693
RX MEDLINE; 97313267.
RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,
RA Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A., Entian K.D.,
RA Floeth M., Goffeau A., Hebling U., Heumann K., Heuss-Neitzel D.,
RA Hilbert H., Hilger F., Kleine K., Kotter P., Louis E.J., Messenguy F.,
RA Mewes H.W., Miosga T., Mostl D., Muller-Auer S., Nentwich U., Obermaier B.,
RA Piravandi E., Pohl T.M., Portetelle D., Purnelle B., Rechmann S.,
RA Rieger M., Rinke M., Rose M., Scharfe M., Scherens B., Scholler P.,
RA Schwager C., Schwarz S., Underwood A.P., Urrestarazu L.A., Vandenbol M.,
RA Verhasselt P., Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R.,
RA Wedler E., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII";
RL Nature 387(6632):0-0(0).
RN [2]
RP 1-15693
RA Geisel C.;
RT "The sequence of S. cerevisiae cosmid 9354";
RL Unpublished.
RN [3]
RP 1-15693
RA Waterston R.;

RT ;
RL Submitted (08-APR-1996) to the EMBL/GenBank/DDBJ databases.
RL Robert Waterston
RN [4]
RP 1-15693
RA Cherry J.M.;

RT ;
RL Submitted (22-AUG-1997) to the EMBL/GenBank/DDBJ databases.
RL Saccharomyces Genome Database
DR SPTREMBL; Q12090; Q12090.
DR SPTREMBL; Q12102; Q12102.
DR SPTREMBL; Q12130; Q12130.
DR SPTREMBL; Q12259; Q12259.
DR SPTREMBL; Q12500; Q12500.
DR SPTREMBL; Q12528; Q12528.
DR SWISS-PROT; P32485; HOG1_YEAST.
DR SWISS-PROT; P38013; PM20_YEAST. . . .

SCORES Init1: 2446 Initn: 2446 Opt: 2446 z-score: 1683.2 E(): 0
99.8% identity in 491 bp overlap

9904247_1.Dn		489	479	469	
		ATGTGATATAGTGTTTAAGCGAATGACAGAAGA			
Scl9354	GATAGAAGCGACAGTAGAAAATTGCATTATTGATATAGTGTTTAAGCGAATGACAGAAGA				
	5140 5150 5160 5170 5180 5190				
	459 449 439 429 419 409				

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9904247_1.Dn TTAATTTCTTGGTATGTTAGGAAAGAATAAAGGAGAATAAGAATAATTAGAACAAATGTAG
Sc19354      |||
              TTAATTTCTTGGTATGTTAGGAAAGAATAAAGGAGAATAAGAATAATTAGAACAAATGTAG
              5200      5210      5220      5230      5240      5250

9904247_1.Dn 399      389      379      369      359      349
Sc19354      GATGGAAAGAAAGATTATCAAGCATGCCGACTTTATATACTTGAACGGAGGCAAAGGATG
              |||
              GATGGAAAGAAAGATTATCAAGCATGCCGACTTTATATACTTGAACGGAGGCAAAGGATG
              5260      5270      5280      5290      5300      5310

9904247_1.Dn 339      329      319      309      299      289
Sc19354      CAAAATTTTCTCACATTTCTTTCTGCCGTTATGTTGGGAGTAAGACTCCCATTATCGCAA
              |||
              CAAAATTTTCTCACATTTCTTTCTGCCGTTATGTTGGAAGTAAGACTCCCATTATCGCAA
              5320      5330      5340      5350      5360      5370

9904247_1.Dn 279      269      259      249      239      229
Sc19354      TACTGCAACACGAATATGCAAATTTGCTGAGTTATCGCAGATAGTTGTTGCAAAGATAG
              |||
              TACTGCAACACGAATATGCAAATTTGCTGAGTTATCGCAGATAGTTGTTGCAAAGATAG
              5380      5390      5400      5410      5420      5430

9904247_1.Dn 219      209      199      189      179      169
Sc19354      CGGCGTAGGTGGCCGCGAAATGGGGAATTCCAAAACAAACGGTTTTTTTACTCCTGAGAA
              |||
              CGGCGTAGGTGGCCGCGAAATGGGGAATTCCAAAACAAACGGTTTTTTTACTCCTGAGAA
              5440      5450      5460      5470      5480      5490

9904247_1.Dn 159      149      139      129      119      109
Sc19354      ATACTTGACGGGATAATCCAGGGCCTACCACCCACGCTTCGAGGATTGGCTTTTATTTT
              |||
              ATACTTGACGGGATAATCCAGGGCCTACCACCCACGCTTCGAGGATTGGCTTTTATTTT
              5500      5510      5520      5530      5540      5550

9904247_1.Dn 99      89      79      69      59      49
Sc19354      TTTTTTTTTTGGTGGCGTTTTATTCTTTCCCGCTTTCTGGGACTTGTGCGGAGTTTTGAG
              |||
              TTTTTTTTTTGGTGGCGTTTTATTCTTTCCCGCTTTCTGGGACTTGTGCGGAGTTTTGAG
              5560      5570      5580      5590      5600      5610

9904247_1.Dn 39      29      19      9
Sc19354      AGGGGCGCGCGGCAAAGGATTCCCAAACGGAAATCAGACG
              |||
              AGGGGCGCGCGGCAAAGGATTCCCAAACGGAAATCAGACG
              5620      5630      5640      5650      5660      5670

Sc19354      GCAGTTCTGGACCCATTCCGATTTTCCCATTGTTCTTGGCGGTGCTGATTCCGACACG
              5680      5690      5700      5710      5720      5730

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9904247_1.Dna /rev
Emfun:Scchxiila

ID SCCHXIILA standard; DNA; FUN; 37639 BP.
AC X89514;
SV X89514.1
DT 03-MAY-1996 (Rel. 47, Created)
DT 14-APR-1997 (Rel. 51, Last updated, Version 4)
DE S.cerevisiae DNA from chromosome XII right arm
KW aspartyl protease; HOG1 gene; mitogen-activated protein kinase;
KW small nuclear RNA U6 protein; SNR6 gene; YAP3 gene.
OS Saccharomyces cerevisiae (baker's yeast)
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;

OC Saccharomycetaceae; Saccharomyces.

RN [1]
 RA Verhasselt P., Volckaert G.;
 RT "Sequence analysis of a 37.6 kbp cosmid clone from the right arm of
 RT Saccharomyces cerevisiae chromosome XII, carrying YAP3, HOG1, SNR6,
 RT tRNA-Arg3 and 23 new open reading frames, among which several homologies
 RT to proteins involved in cell division control and to mammalian growth
 RT factors and other animal proteins are found";
 RL Yeast 13:241-250(1997).
 RN [2]
 RA Volckaert G.;
 RT ;
 RL Submitted (07-JUL-1995) to the EMBL/GenBank/DDBJ databases.
 RL G. Volckaert, Laboratory of Gene Technology, Catholic University of Leuven,
 RL Willem de Croylaan, B-3001 Leuven, BELGIUM
 RN [3]
 RP 1-37639
 RA Volckaert G.;
 RT ;
 RL Submitted (20-SEP-1995) to the EMBL/GenBank/DDBJ databases.
 RL G. Volckaert, Laboratory of Gene Technology, Catholic University of Leuven,
 RL Willem de Croylaan 42, B-3001 Leuven, BELGIUM
 DR SPTREMBL; Q05382; Q05382.
 DR SPTREMBL; Q05383; Q05383.
 DR SPTREMBL; Q05385; Q05385.
 DR SPTREMBL; Q12090; Q12090.
 DR SPTREMBL; Q12102; Q12102.
 DR SPTREMBL; Q12130; Q12130.
 DR SPTREMBL; Q12138; Q12138.
 DR SPTREMBL; Q12174; Q12174.
 DR SPTREMBL; Q12186; Q12186.
 DR SPTREMBL; Q12259; Q12259.
 DR SPTREMBL; Q12288; Q12288.
 DR SPTREMBL; Q12309; Q12309.
 DR SPTREMBL; Q12312; Q12312.
 DR SPTREMBL; Q12354; Q12354.
 DR SPTREMBL; Q12395; Q12395.
 DR SPTREMBL; Q12440; Q12440.
 DR SPTREMBL; Q12500; Q12500.
 DR SPTREMBL; Q12528; Q12528. . . .

SCORES Initl: 2446 Initn: 2446 Opt: 2446 z-score: 1679.7 E(): 0
 99.8% identity in 491 bp overlap

9904247_1.Dn
 ATGTGATATAGTGTTTAAGCGAATGACAGAAGA
 |||||||||||||||||||||||||||||||||||
 Scchxiila GATAGAAGCGACAGTAGAAAATTGCATTATTGATATAGTGTTTAAGCGAATGACAGAAGA
 6680 6690 6700 6710 6720 6730
 9904247_1.Dn TTAATTTCTTGGTATGTTAGGAAAGAAATAAGGAGAATAAGAATAATTAGAACAATGTAG
 |||||||||||||||||||||||||||||||||||
 Scchxiila TTAATTTCTTGGTATGTTAGGAAAGAAATAAGGAGAATAAGAATAATTAGAACAATGTAG
 6740 6750 6760 6770 6780 6790
 9904247_1.Dn GATGGAAAGAAAGATTATCAAGCATGCCGACTTTATATACTTGAACGGAGGCAAAGGATG
 |||||||||||||||||||||||||||||||||||
 Scchxiila GATGGAAAGAAAGATTATCAAGCATGCCGACTTTATATACTTGAACGGAGGCAAAGGATG
 6800 6810 6820 6830 6840 6850
 339 329 319 309 299 289

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9904247_1.Dn CAAAATTTTCTCACATTTCTTTCTGCCGTTATGTTGGGAGTAAGACTCCCATTATCGCAA
|||
Scchxiila CAAAATTTTCTCACATTTCTTTCTGCCGTTATGTTGGAAGTAAGACTCCCATTATCGCAA
6860 6870 6880 6890 6900 6910

279 269 259 249 239 229
9904247_1.Dn TACTGCAACACGAATATGCAAATTTGCTGAGTTATCGCAGATAGTTGTTGCAAAGATAG
|||
Scchxiila TACTGCAACACGAATATGCAAATTTGCTGAGTTATCGCAGATAGTTGTTGCAAAGATAG
6920 6930 6940 6950 6960 6970

219 209 199 189 179 169
9904247_1.Dn CGGCGTAGGTGGCCGCGAAATGGGGAATTCCAAAACAAACGGTTTTTTTACTCCTGAGAA
|||
Scchxiila CGGCGTAGGTGGCCGCGAAATGGGGAATTCCAAAACAAACGGTTTTTTTACTCCTGAGAA
6980 6990 7000 7010 7020 7030

159 149 139 129 119 109
9904247_1.Dn ATACTTGTACGGGATAATCCAGGGCCTACCACCCACGCTTCGAGGATTGGCTTTTATTTT
|||
Scchxiila ATACTTGTACGGGATAATCCAGGGCCTACCACCCACGCTTCGAGGATTGGCTTTTATTTT
7040 7050 7060 7070 7080 7090

99 89 79 69 59 49
9904247_1.Dn TTTTTTTTTTGGTGGCGTTTTATTTCTTTCCCGCTTTCTGGGACTTGTGCGGAGTTTTGAG
|||
Scchxiila TTTTTTTTTTGGTGGCGTTTTATTTCTTTCCCGCTTTCTGGGACTTGTGCGGAGTTTTGAG
7100 7110 7120 7130 7140 7150

39 29 19 9
9904247_1.Dn AGGGGCGCGCGGCAAAGGATTCCCAAACGGAATCAGACG
|||
Scchxiila AGGGGCGCGCGGCAAAGGATTCCCAAACGGAATCAGACGCCAATAGCCAGCACTCAAA
7160 7170 7180 7190 7200 7210

Scchxiila GCAGTTCTGGACCCATTCCGATTTTCCCATTTGTTTCTTGCGCGTGCTGATTCCGACACG
7220 7230 7240 7250 7260 7270

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9904247_1.Dna
Emgss6:Aq492301

ID AQ492301 standard; DNA; GSS; 630 BP.
AC AQ492301;
SV AQ492301.1

DT 27-APR-1999 (Rel. 59, Created)
DT 04-MAR-2000 (Rel. 63, Last updated, Version 2)
DE V119H10 mTn-3xHA/lacZ Insertion Library *Saccharomyces cerevisiae* genomic
DE 5', genomic survey sequence.
KW GSS.
OS *Saccharomyces cerevisiae* (baker's yeast)
OC Eukaryota; Fungi; Ascomycota; *Saccharomycetes*; *Saccharomycetales*;
OC *Saccharomycetaceae*; *Saccharomyces*.
RN [1]
RP 1-630
RA Ross-Macdonald P., Roemer T., Coelho P.S.R., Agarwal S., Kumar A.,
RA desEtages S.A., Cheung K.-H., Sheehan A., Symoniatis D., Jansen R.,
RA Umansky L., Heidtman M., Nelson K., Iwasaki H., Kanada D., Lugo R.,
RA Hager K., Miller P., Roeder G.S., Snyder M.;
RT "Large-Scale Analysis of the Yeast Genome by Transposon Tagging and Gene
RT Disruption";
RL Unpublished.
CC Contact: Kumar A
CC Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
CC Yale University